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21. Use of a nucleic acid according to Claim 1, of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to Claim 13, or of a pharmaceutical composition according to Claim 19 for preparing an agent for exerting an effect on the binding of fibrinogen to blood platelets.

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25. Process according to Claim 23, characterized in that the antibody-encoding nucleic acids are used for expressing recombinant antibody chains, or derivatives or fragments thereof.

REMARKS

In accordance with 37 C.F.R. 1.821(C), Applicants submit herewith the Sequence Listing for the above-identified application both in paper copy form and in computer readable form.

The name of the file on the computer readable form is 05649049.APP. The paper copy and the computer readable copy are the same.

Claims 1-25 are currently pending. In response to the Examiner's request made during a telephone interview on April 18, 2001, claims 3, 6, 11, 12, 13, 16, 17, 19, 20, 21 and 25 are amended herein to eliminate multiple dependencies. Claims 1-25, as amended, are presented for reconsideration.

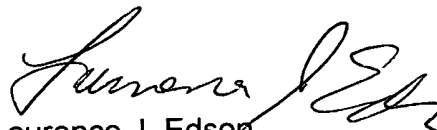
In view of the amendments and remarks above, Applicants submit that this application is in condition for examination on the merits and request consideration and favorable action thereon.

If for any reason, the Examiner feels the application is not now in condition for examination, it is respectfully requested that the Examiner contact, by telephone, Applicants' undersigned attorney at the indicated telephone number to arrange for an interview to expedite the disposition of this application.

In the event this paper is not considered to be timely filed, Applicants hereby petition for an appropriate extension of time. The fee for this extension may be charged to our Deposit Account No. 01-2300, along with any other fees which may be required with respect to this paper.

Respectfully submitted,

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Enclosures: Marked-Up Copy of Claims
Substitute Tables 3, 6, 7a and 7b
Petition for Extension of Time
Sequence Listing

MARKED-UP CLAIMS

3. (Twice Amended) Nucleic acid according to [either] Claim 1 [or 2],
which furthermore comprises a CDR2 region, selected from:

- (a) a nucleotide sequence which encodes the amino acid sequence:

D I S Y S G S T K Y K P S L R S, (SEQ ID NO:35)

- (b) a nucleotide sequence which encodes the amino acid sequence:

V I S Y D G S N K Y Y A D S V K G, (SEQ ID NO:36)

and

- (c) a nucleotide sequence which encodes an amino acid sequence
having an homology of at least 80% with an amino acid
sequence from (a) or (b).

6. (Twice Amended) Nucleic acid according to Claim 4 [or 5], which
furthermore comprises a CDR2 region selected from:

- (a) a nucleotide sequence which encodes the amino acid sequence:

G S H Q R P S, (SEQ ID NO:41)

- (b) a nucleotide sequence which encodes the amino acid sequence:

S N N Q R P S, (SEQ ID NO:42)

and

- (c) a nucleotide sequence which encodes an amino acid sequence
having an homology of at least 80% with an amino acid
sequence from (a) or (b).

11. Vector, characterized in that it

- (a) contains at least one copy of a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or at least one copy of a nucleic acid according to [one of Claims] Claim 4 [to 6] or
- (b) contains at least one copy of a nucleic acid according to Claim 7 [or 8] and/or at least one copy of a nucleic acid according to [Claims] Claim 9 [or 10].

12. Cell, characterized in that it

- (a) expresses a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or a nucleic acid according to [one of Claims] Claim 4 [to 6] or
- (b) a nucleic acid according to Claim 7 [or 8] and/or a nucleic acid according to Claim 9 [or 10].

13. Polypeptide, characterized in that it

- (a) is encoded by a nucleic acid according to [one of Claims] Claim 1 [to 3] and/or a nucleic acid according to [one of Claims] Claim 4 [to 8] or
- (b) by a nucleic acid according to Claim 7 [or 8] and/or a nucleic acid according to Claim 9 [or 10].

16. Polypeptide according to [one of Claims] Claim 13 [to 15],
characterized in that it is coupled to a labelling group or a toxin.

17. Antibody against a polypeptide according to [one of Claims] Claim 13
[to 16].

19. Pharmaceutical composition which comprises, as the active
component, a nucleic acid according to [one of Claims] Claim 1 [to 10], a vector
according to Claim 11, a cell according to Claim 12, a polypeptide according to [one of
Claims] Claim 13 [to 16] or an antibody according to [either] Claim 17 [or 18], where
appropriate together with other active components and pharmaceutically customary
adjuvants, additives or excipients.

20. Use of a nucleic acid according to [one of Claims] Claim 1 [to 10], of a
vector according to Claim 11, of a cell according to Claim 12, of a polypeptide
according to [one of Claims] Claim 13 [to 16], of an antibody according to Claim 17 [or
18], or of a pharmaceutical composition according to Claim 19 for preparing an agent
for the diagnosis or for the treatment or prevention of AITP.

21. Use of a nucleic acid according to [one of Claims] Claim 1 [to 10], of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to [one of Claims] Claim 13 [to 16], or of a pharmaceutical composition according to Claim 19 for preparing an agent for exerting an effect on the binding of fibrinogen to blood platelets.

25. Process according to Claim 23 [or 24], characterized in that the antibody-encoding nucleic acids are used for expressing recombinant antibody chains, or derivatives or fragments thereof.

Table 3

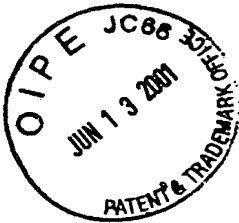
A. Heavy Chains

Heavy Chains		A.													
Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4	
VH4.11	2	QVQLQESGRLVKPSRSLTCTVSGGIS	SYVWS	WIRPPKGLEWIG	YIYSGSTNYNPSLKS	D-S-----K-K--R-	RVTSVDTSKNQFSLKLSSTAADTAIVYICAR	VLPPDPISMDV	WGKGTITVTSS						
PDG7		--K-L-----N--R--	G-S-R	---S-----	---	---	---	---	---						
PDG8		---	---	---	---	---	---	---	---						
PDG10		---	---	---	---	---	---	---	---						
PDG16		---	---	---	---	---	---	---	---						
1.9III	6	QVQLVESGGGVQPGRSRLSCAASGETES	SYGMH	WVRQAPKGLEWVA	VISYDGSNKYYADSVKG	---	RTTISRDNKNTLYLQMNLSRAEDTAIVYICAK	ALGSGGGWDHYMDV	WGKGTITVTSS						
PDG13		--K-L-----	--A--	---	---	---	--A-----R	---	WGKGTITVTSS						
PDG17		---	---	---	---	---	---	---	WGKGTITVTSS						
PDG31		---	---	---	---	---	---	---	WGKGTITVTSS						
PDG37		---	---	---	---	---	---	---	WGKGTITVTSS						
H85255		---	---	---	---	---	---	---	WGQGTITVTSS						

B. Light Chains

Clones	SEQ ID	FR1	ID	CDR1	ID	FR2	ID	CDR2	ID	FR3	ID	CDR3	ID	FR4
DPL2	4	VLTPPSASGTPGQRTISC		SGSSNIGSNTVH		WYQQLPGTAPKLLIY		SNNQRPS		GVPDRFSGSKGTSASLATISGLQSEDEADYYC		AAWDDSLNG		FGGGTKLTVLSQP
PDG7		-V-----W----		-----R--P-S		--H-V-----F		GSH----		-----R-----G-AG----		-T---G---PV		FGGGTKLTVLSQP
PDG8		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP
PDG10		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP
PDG16		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP
DPL2	8	VLTPPSASGTPGQRTISC		SGSSNIGSNTVN		WYQQLPGTAPKLLIY		SNNQRPS		GVPDRFSGSKGTSASLATISGLQSEDEADYYC		AAWDDSLNG		FGGGTKLTVLSQP
PDG13		-V-----		-----		-----		-----		-----		-----WV		FGGGTKLTVLSQP
PDG17		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP
PDG31		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP
PDG37		-----		-----		-----		-----		-----		-----		FGGGTKLTVLSQP

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (VH4.11; 1.9III; DPL2) are given for comparative purposes and in each case represent the deduced amino acid sequence for the most closely related published strainline gene sequence. Dashes denote identity. M85255 refers to the EMPL/GenBank reference number and denotes the deduced amino acid sequence of the human anti-GPIIb autoantibody 2E7 (Kunicki et al., J. Autoimmun. 4 (1991), 433-446). In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of PDG7 and PDG13 are presented in SEQ ID NO:2 and 6, respectively. The amino acid sequences of the light chains of PDG7 and PDG13 are presented in SEQ ID NO:4 and 8, respectively.



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Table 6

anti-Id phage clones antiidiotypic phab clones (AI-X and AI-B)	H Chain				L Chain			
	Seq. ID No (s).	V _H family	Straightline Gene	Homology (%) *	Seq. ID No (s).	V _L family	Strainline gene	Homology (%) *
AI-X16	10, 54, 74, 75, 43	V _H 3	DP47	88	12, 80, 81	V _L 2	DPL10	88
AI-X24	-	V _H 3	DP47	88	-	V _L 2	DPL10	88
AI-X17	76	V _H 3	DP47	87	-	V _L 2	DPL10	88
AI-X39	16, 55, 77, 44	V _H 3	DP49	94	-	-	-	-
AI-X40	123, 56, 78, 45	V _H 3	DP31	95	-	-	-	-
AI-X20	14, 57, 79, 46	V _H 4	DP71	78	-	-	-	-
AI-B14	22, 83, 84, 85	V _H 3	DP46	91	-	-	-	-
AI-B17	-	V _H 3	DP46	91	-	-	-	-
AI-B18	24, 86, 87, 88	V _H 1	DP10	85	-	-	-	-
AI-B24	26, 127, 88, 89	V _H 3	DP49	81	122, 116, 99	V _L 3	3h	82
AI-B38	30, 94, 98, 90	V _H 1	DP5	98	-	-	-	-

* Highest homology (in %) of the amino acid sequences of the respective phab clones with sequences of known strainline V genes

Table 7a

A. Heavy Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
DP47		EVQLVESGGGLVQPGGSLRLSCAASGFTFS	103	SYAMS		WVRQAPGKGLEWVS	107	AISGSGSTYYADSVKSG		RTTISRDNKNTLYLQWNSLRAEDTAVYYCAK				
AIX16	10	Q-K-----H-----D	54	NF--		-----	74	G--G-LL-H-----	75	-----N--R--V-----	43	VRDLGVRVLSTFTFDI		WQGGTKVTVSS
AIX24		-----				-----		-----		-----		-----		-----
AIX17		-----				-----		-----N-----		-----		-----		-----
DP49		QVQLVESGGGVQPGGSLRLSCAASGFTFS	104	SYGMH		WVRQAPGKGLEWVA	108	VISYDGSNKYYADSVKSG		RTTISRDNKNTLYLQWNSLRAEDTAVYYCAK				
AIX39	16	--K-L-----H-----	55	--T--		-----	77	L-----		-----A-----K-----	44	DGRSGSYAREFDGMDV		WQGGTTVTVSS
DP31		EVQLVESGGGLVQPGGSLRLSCAASGFTFD	105	DYAMH		WVRQAPGKGLEWVS	109	GISWNSGSGYADSVKSG		RTTISRDNKNTLYLQWNSLRAEDTAVYYCAK				
AIX40	123	--K-L-----	56	---L-		-----	78	---D-T-----		-----	45	MGSSVVATYNAEDI		WQGGTMVTVSS
DP71		QVQLQESGGPELVKPSSETLSLTCTVSGGSIS	106	SYWS		WIRQPPGKGLEWIG	110	YIYSGSTNYNPSLKS		RVTISVDTSKNTLYLQWNSLRAEDTAVYYCAR				
AIX20	14	--K-L-----DV--R	57	-H--		-L-----	79	F--DGAR-RF-----R-		---SL-M-P-K-----G-----S-----	46	DADGGFSPYYFPY		WQGGIPVSVSS

B. Light Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
DPL10		QSALTQPASVSGSPGQSITISC	124	TGTSSDVGSYNLVS		WYQHHPGKAPKLMY	125	EVSKRPS		GVSNRFSGSKGNTASLTISGLQAEDEADYYC	126	CSYAGSSTF		
AIX16	12	VV-----	80	---AI-N--F-P		-----	81	-G-----		-----E--	82	---VH---N		WVFGGTKLTVLGQPKAARSVTLFFPSS
AIX24		-----				-----		-----		-----		-----		-----
AIX17		-----				-----		-----		-----		-----		-----

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (DP47, DP49, DP31, DP71 and DPL10) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of AIX16, AIX39, AIX40, and AIX20 are presented in SEQ ID NO:10, 16, 123 and 14, respectively. The amino acid sequences of the CDR1 regions of the heavy chains of AIX16, AIX39, AIX40, AIX20, DP47, DP49, DP31 and DP71 are presented in SEQ ID NO:54, 55, 56, 57, 103, 104, 105 and 106, respectively. The amino acid sequences of the CDR2 regions of the heavy chains of AIX16, AIX17, AIX39, AIX40, AIX20, DP47, DP49, DP31 and DP71 are presented in SEQ ID NO:74, 76, 77, 78, 79, 107, 108, 109 and 110, respectively. The amino acid sequence of the light chain of AIX16 is presented in SEQ ID NO:12. The amino acid sequences of the DCR1, CDR2 and CDR3 regions of AIX16 are presented in SEQ ID NO:80, 81, and 82, respectively. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of DPL10 are presented in SEQ ID NO:124, 125 and 126, respectively.

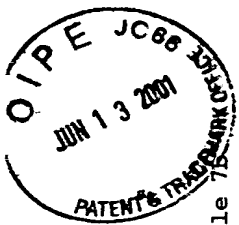


Table 75

A. Heavy Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
DP46	22	QVQLVESGGGVQPGRLSLRSCAASGFTFS	91	SYAMH	95	WVRQAPGKGLEWVA	95	VISYDGSNKYYADSVKRG	95	RTTISRDNSTNTLYLQMNLSRAEDTAVYYCAR	85	DSETAIAAAGREFDI	85	WQGGTMTVTSS
AI-B14	22	--K-L-	83	D-G--	84	-----	84	A-----	84	--S-----N-----ST-----F--	85	-----	85	-----
AI-B17	22	-----	83	-----	84	-----	84	-----	84	-----	85	-----	85	-----
DP-10	24	QVQLVQSGAEVVKPGSSVKVSKASGGTFS	92	SYAIS	96	WVRQAPGQGLEWMG	96	GIPIFGTANYAQKFOG	96	RVTITADESTSTAYMELSLRSLEDTAVYYCAR	88	EDGTTVPSPQLEF	88	WQGGTRVTVSS
AI-B18	24	--K-LE-	86	-HT--	87	-----	87	--T-----V-----	87	-----P-----R--T--DSGI-----	88	-----	88	-----
DP-49	26	QVQLVESGGGVQPGRLSLRSCAASGFTFS	93	SYGMH	97	WVRQAPGKGLEWVA	97	VISYDGSNKYYADSVKRG	97	RTTISRDNSTNTLYLQMNLSRAEDTAVYYCAR	89	SGSGYLGYFYDY	89	WQGGTTLTVSS
AI-B24	26	--K-L--L--G-----S-----N	127	K-AI-	88	-----Y-S	88	A--SN-G-T-----	88	-----V-----S-----VR	89	-----	89	-----
DP-5	30	QVQLVQSGAEVVKPGASVKVSGYTLT	94	ELSMH	98	WVRQAPGKGLEWMG	98	GFDPEDGETIYVAKKFOG	98	RVTMTEDTSTDTAYMELSLRSLEDTAVYYCAT	90	GLRSYNYGRNLDY	90	WQGGTTLTVSS
AI-B38	30	Q-K-LE-	94	-----	98	-----	98	-----	98	-----	90	-----	90	-----

B. Light Chains

Clones	SEQ ID	FR1	SEQ ID	CDR1	SEQ ID	FR2	SEQ ID	CDR2	SEQ ID	FR3	SEQ ID	CDR3	SEQ ID	FR4
VL3h	100	SYVLTPSPSVSVARPKTARITC	100	GNNGIGSKSVH	101	YSDRPS	101	FIPERFSGSGSGNTATLTISRVEAGDEADYYC	102	QWSSSSSDH	99	-----NTN-Q	99	TIFGGGTKLTVLRQPKAAPSVTLFPPSS
AI-B24	122	--V-----RQ--T---	122	--YK-----	116	E--Y---	116	E-----	102	QWSSSSSDH	99	-----	99	-----

FR: Framework region; CDR: complement-determining [sic] region. The top sequences (DP46, DP10, DP49, DP5 and VL3h) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence. The amino acid sequences of the heavy chains of A-B14, AI-B18, AI-B24 and AI-B38 are presented in SEQ ID NO:22, 24, 26 and 30, respectively. The amino acid sequences of the CDR1 regions of the heavy chains of AI-B14, AI-B18, AI-B24, AI-B38, DP-46, DP-10, DP-49 and DP-5 are presented in SEQ ID NO:83, 86, 127, 94, 91, 92, 93 and 94, respectively. The amino acid sequences of the CDR2 regions of the heavy chains of AI-B14, AI-B18, AI-B24, AI-B38, DP-46, DP-10, DP-49 and DP-5 are presented in SEQ ID NO:84, 87, 88, 95, 96, 97 and 98, respectively. The amino acid sequence of CDR3 regions of the heavy chains of AI-B14, AI-B18, AI-B24, and AI-B38 are presented in SEQ ID NO:85, 88, 89 and 90, respectively. The amino acid sequences of the light chain of AI-B24 is presented in SEQ ID NO:28. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of the light chains of AI-B24 are presented in SEQ ID NO:122, 116 and 99, respectively. The amino acid sequences of the CDR1, CDR2 and CDR3 regions of the light chains of VL3h are presented in SEQ ID NO:100, 101 and 102, respectively.